

10/525,743

Sequence Alignments

/JML/

RESULT 8

AAP80269

ID AAP80269 standard; protein; 212 AA.

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AC AAP80269;

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DT 15-JUN-2007 (revised)

DT 25-MAR-2003 (revised)

DT 03-OCT-2002 (revised)

DT 08-OCT-1990 (first entry)

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DE Recombinant interleukin 6.

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KW IL-6; interleukin; cancer; BOND_PC; interleukin 6 (interferon, beta 2);

KW interleukin 6 (interferon, beta 2) [Homo sapiens]; IL6; HGF; HSF; BSF2;

KW IL-6; IFNB2; interleukin 6 (interferon, beta 2), isoform CRA_a;

KW interleukin 6 (interferon, beta 2), isoform CRA_a [Homo sapiens];

KW unknown; unknown [Homo sapiens]; interleukin-6;

KW interleukin-6 [Homo sapiens]; interferon 6 precursor; interleukin 6;

KW hybridoma growth factor peptide; interleukin 6 [Homo sapiens];

KW unnamed protein product; unnamed protein product [Homo sapiens];

KW put. mature polypeptide (AA 1-184); IL6 [Homo sapiens];

KW B cell stimulatory factor-2 (BSF-2);

KW B cell stimulatory factor-2 (BSF-2) [Homo sapiens];

KW interleukin 6 [synthetic construct];

KW interleukin 6 (interferon, beta 2) [synthetic construct]; GO1781; GO5125;

KW GO5138; GO5515; GO5576; GO5615; GO6953; GO6959; GO7166; GO7267; GO8284;

KW GO8285; GO43066; GO45079; GO45630; GO45727.

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OS Homo sapiens.

OS Synthetic.

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FH Key Location/Qualifiers

FT Peptide 1. .27

FT /label= signal peptide

FT Modified-site 73. .75

FT /label= Glycosylation site

FT /note= "N-linked"

FT Modified-site 172. .174

FT /label= Glycosylation site

FT /note= "N-linked"

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PN WO8800206-A.

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PD 14-JAN-1988.

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PF 07-JUL-1987; 87WO-US001611.

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PR 08-JUL-1986; 86US-00883207.

PR 15-JUL-1986; 86US-00885905.

PR 08-MAY-1987; 87US-00047957.

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PA (GEMY) GENETICS INST INC.

PI Clark SC, Wong GG, Schendel P, Mccoy J;
 XX
 DR WPI; 1988-021566/03.
 DR N-PSDB; AAN80299.
 DR PC:NCBI; gi10834984.
 DR PC:SWISSPROT; P05231.
 DR PC:BIND; 116560,179493,116559,179102,262686,227104,179037.
 XX
 PT Prodn. of non-glycosylated IL-6 - for use in treatment of deficiency
 PT disorders in haematopoietic cells and in cancer therapy.
 XX
 PS Disclosure; Page ?; -pp; English.
 XX
 CC The sequence is encoded by DNA carried by pCSF309 in E.coli MC1061 (ATCC
 CC 67153) as an EcoRI insert. This can be excised and used to construct an
 CC expression plasmid for prodn. of IL-6. Bacterially produced IL-6 is non-
 CC glycosylated. It can be used against diseases caused by decreased levels
 CC of either myeloid or lymphoid cells of the haematopoietic system. It may
 CC also be used in conjunction with other interleukin therapies or as a
 CC hybridoma growth factor in culture medium. See also AAP80270. (Updated on
 CC 03-OCT-2002 to add missing OS field.) (Updated on 25-MAR-2003 to correct
 CC PR field.) (Updated on 25-MAR-2003 to correct PA field.)
 CC
 CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed
 CC information from BOND.
 XX
 SQ Sequence 212 AA;

Query Match 94.7%; Score 790.5; DB 1; Length 212;
 Best Local Similarity 76.4%; Pred. No. 4.1e-73;
 Matches 162; Conservative 0; Mismatches 1; Indels 49; Gaps 1;

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Qy      1 MNSFSTSAFGPVAFSLGLLLVLPAAFPAPVPPGEDSKDVAAPHRQPLTSSERIDKQIRYI 60
      |||
Db      1 MNSFSTSAFGPVAFSLGLLLVLPAAFPAPVPPGEDSKDVAAPHRQPLTSSERIDKQIRYI 60

Qy     61 LDGISALRKETCNKSNMCESKEALAENNPNLPKMAEKDGCQSGFNE----- 108
      |||
Db     61 LDGISALRKETCNKSNMCESKEALAENNLNLPKMAEKDGCQSGFNEETCLVKIITGLL 120

Qy    109 -----AKNLDAITTPDPTTNASLLTKLQ 131
      |||
Db    121 EFEVYLEYLQNRFESSEEQARAVQMSTKVLIQFLQKKAKNLDAITTPDPTTNASLLTKLQ 180

Qy    132 AQNQWLQDMTTHLILRSFKEFLQSSLRALRQM 163
      |||
Db    181 AQNQWLQDMTTHLILRSFKEFLQSSLRALRQM 212
  
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Alignment Scores:

Pred. No.:	1.59e-73	Length:	212
Score:	790.50	Matches:	162
Percent Similarity:	76.4%	Conservative:	0
Best Local Similarity:	76.4%	Mismatches:	1
Query Match:	45.1%	Indels:	49
DB:	1	Gaps:	1

US-10-525-743A-2 (1-962) x AAP80269 (1-212)

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Qy      34 ATGAACTCCTTCTCCACAAGCGCCTTCGGTCCAGTTGCCTTCTCCCTGGGGCTGCTCCTG 93
          |||
Db      1 MetAsnSerPheSerThrSerAlaPheGlyProValAlaPheSerLeuGlyLeuLeuLeu 20

Qy      94 GTGTTGCCTGCTGCCTTCCCTGCCCCAGTACCCCCAGGAGAAGATTCCAAAGATGTAGCC 153
          |||
Db     21 ValLeuProAlaAlaPheProAlaProValProProGlyGluAspSerLysAspValAla 40

Qy     154 GCCCCACACAGACAGCCACTCACCTCTTCAGAACGAATTGACAAACAAATTCGGTACATC 213
          |||
Db     41 AlaProHisArgGlnProLeuThrSerSerGluArgIleAspLysGlnIleArgTyrIle 60

Qy     214 CTCGACGGCATCTCAGCCCTGAGAAAGGAGACATGTAACAAGAGTAACATGTGTGAAAGC 273
          |||
Db     61 LeuAspGlyIleSerAlaLeuArgLysGluThrCysAsnLysSerAsnMetCysGluSer 80

Qy     274 AGCAAAGAGGCACTGGCAGAAAACAACCCGAACCTTCCAAAGATGGCTGAAAAAGATGGA 333
          |||
Db     81 SerLysGluAlaLeuAlaGluAsnAsnLeuAsnLeuProLysMetAlaGluLysAspGly 100

Qy     334 TGCTTCCAATCTGGATTCAATGAG----- 357
          |||
Db    101 CysPheGlnSerGlyPheAsnGluGluThrCysLeuValLysIleIleThrGlyLeuLeu 120

Qy     357 ----- 357

Db    121 GluPheGluValTyrLeuGluTyrLeuGlnAsnArgPheGluSerSerGluGluGlnAla 140

Qy     358 -----GCAAAGAAT 366
          |||
Db    141 ArgAlaValGlnMetSerThrLysValLeuIleGlnPheLeuGlnLysLysAlaLysAsn 160

Qy     367 CTAGATGCAATAACCACCCCTGACCCAACCACAAATGCCAGCCTGCTGACGAAGCTGCAG 426
          |||
Db    161 LeuAspAlaIleThrThrProAspProThrThrAsnAlaSerLeuLeuThrLysLeuGln 180

Qy     427 GCACAGAACCAGTGGCTGCAGGACATGACAACTCATCTCATTCTGCGCAGCTTTAAGGAG 486
          |||
Db    181 AlaGlnAsnGlnTrpLeuGlnAspMetThrThrHisLeuIleLeuArgSerPheLysGlu 200

Qy     487 TTCCTGCAGTCCAGCCTGAGGGCTCTTCGGCAAATG 522
          |||
Db    201 PheLeuGlnSerSerLeuArgAlaLeuArgGlnMet 212
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